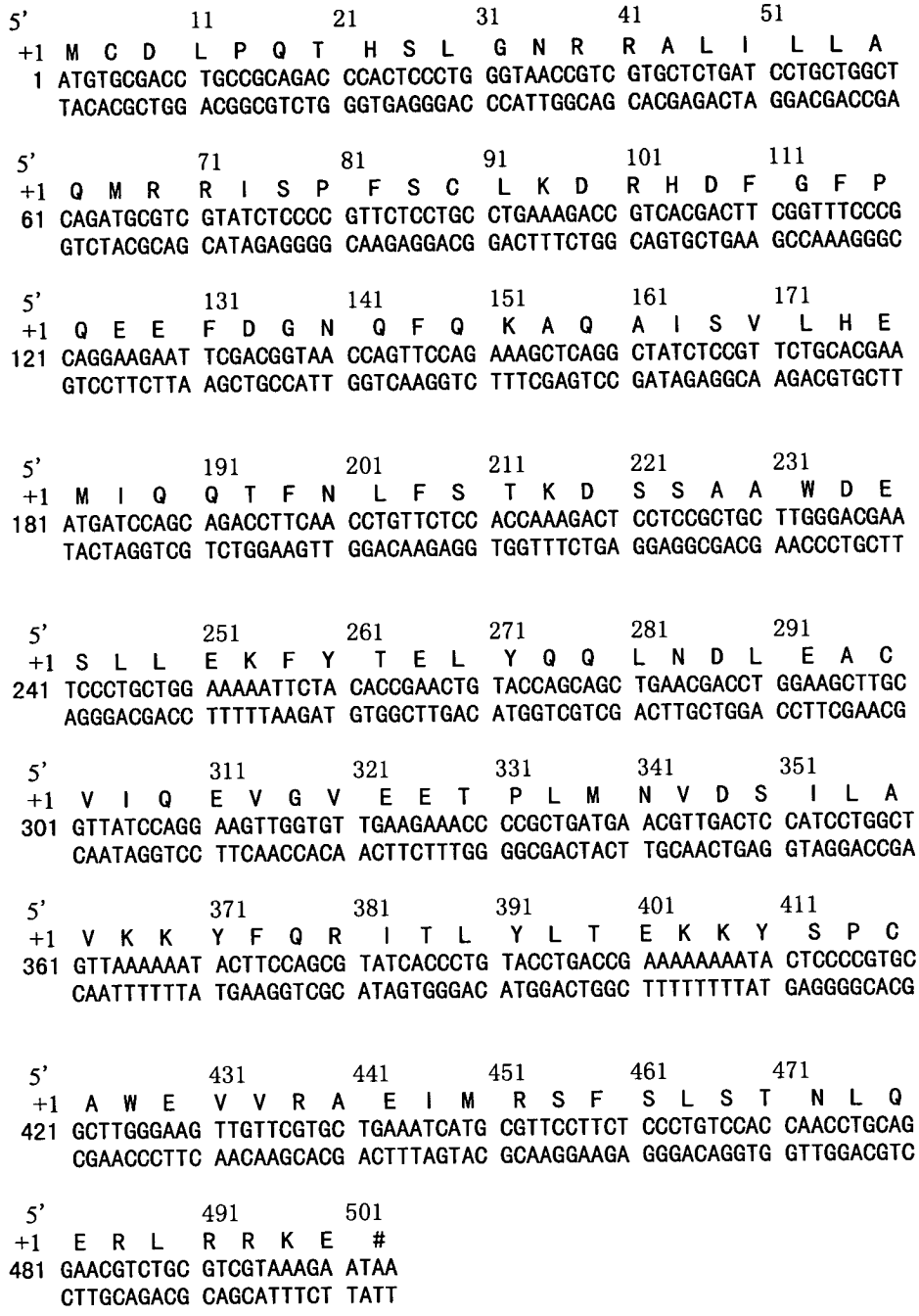
Figure 1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5' 71 81 91 101 111
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5' 131 141 151 161 171
+1 Q E E F D G N Q F Q K A Q A I S V L H E
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GTCCTTCTTA AGCTGCCATT GGTCAAGGTC TTTCGAGTCC GATAGAGGCA AGACGTGCTT
5' 191 201 211 221 231
+1 M I Q Q T F N L F S T K D S S A A W D E
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TACTAGGTCG TCTGGAAGTT GGACAAGAGG TGGTTTCTGA GGAGGCGACG AACCCTGCTT
5' 251 261 271 281 291
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5' 371 381 391 401 411
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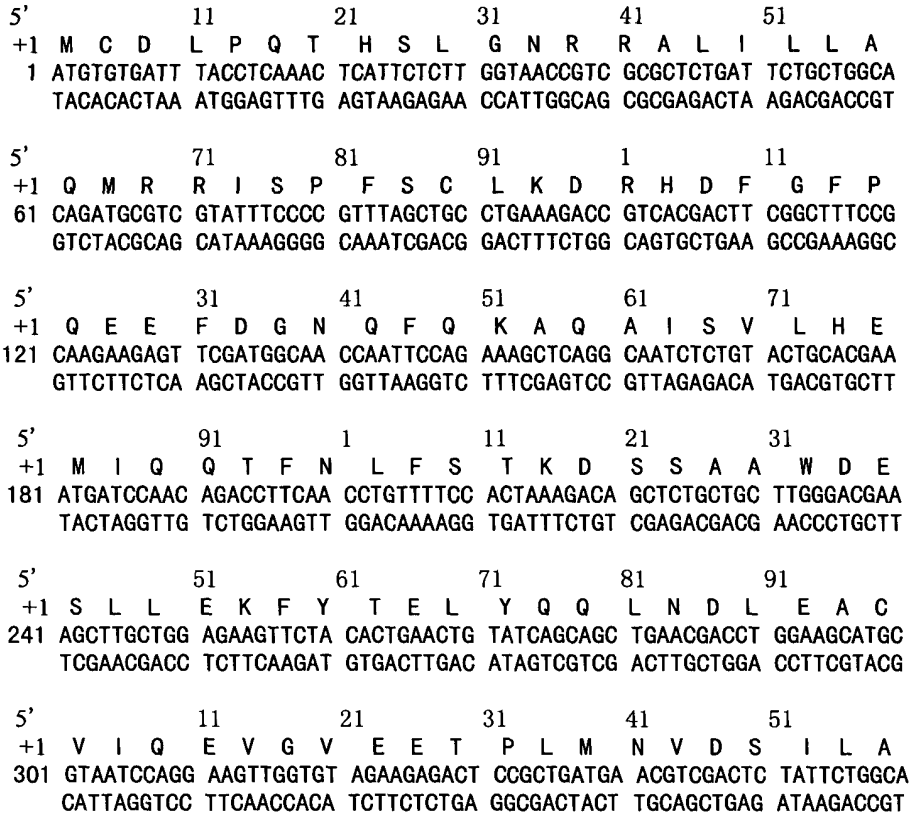
Figure 2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5' 31 41 51 61 71
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5' 91 1 11 21 31
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5' 51 61 71 81 91
+1 S L L E K F Y T E L Y Q Q L N D L E A C
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5' 11 21 31 41 51
+1 V I Q E V G V E E T P L M N V D S I L A
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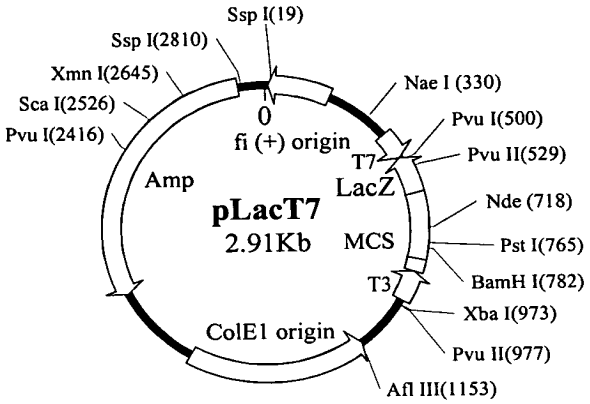
Figure 3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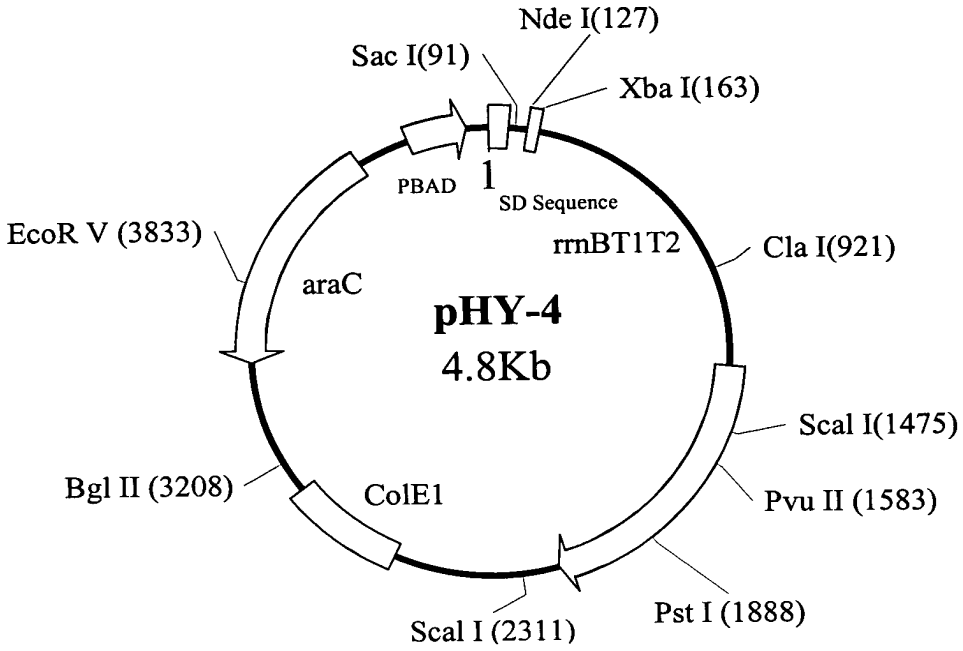
Xmn I(2645)
Sca I(2526)
Pvu I(2416)
Nae I (330)
Pvu I(500)
Pvu II(529)
Nde (718)
Pst I(765)
BamH I(782)
Xba I(973)
Pvu II(977)
Afl III(1153)
0
fi (+) origin
T7
LacZ
MCS
T3
Amp
pLacT7
2.91Kb
ColE1 origin

Figure 4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Sac I(91)
Xba I(163)
PBAD
1
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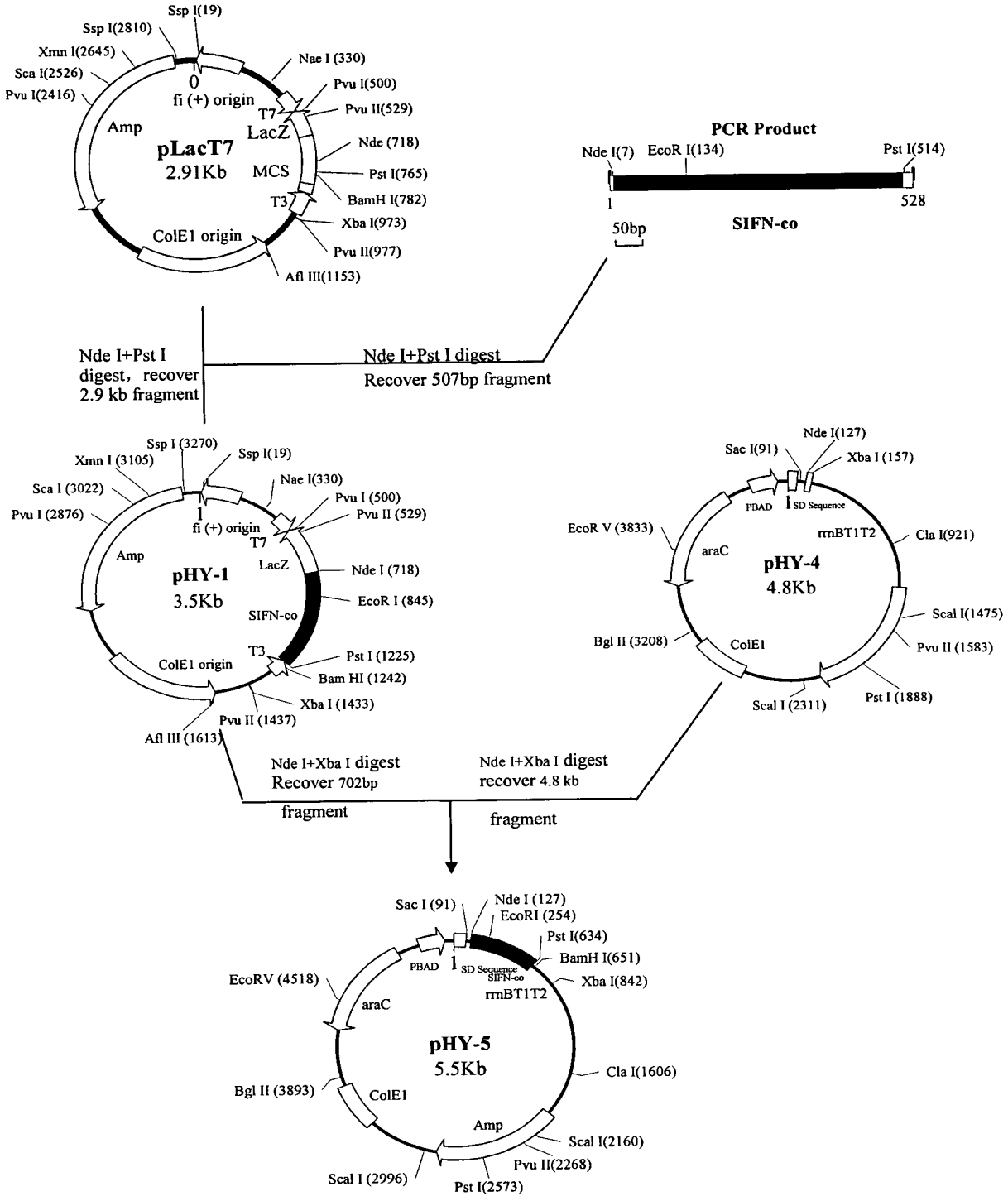
Cla I(921)
araC
pHY-4
4.8Kb
ScaI I(1475)
Bgl II (3208)
ColE1
Pvu II (1583)
ScaI I (2311)
Pst I (1888)

Figure 5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Ssp I(2810)
Xmn I(2645)
Sca I(2526)
Pvu I(2416)
Nae I (330)
Pvu I(500)
Pvu II(529)
Nde (718)
Pst I(765)
BamH I(782)
Xba I(973)
Pvu II(977)
Afl III(1153)
0
fi (+) origin
T7
LacZ
Amp
pLacT7
2.91Kb
MCS
T3
ColE1 origin
PCR Product
Nde I(7)
EcoR I(134)
Pst I(514)
1
528
50bp
SIFN-co
Nde I+Pst I digest
Recover 507bp fragment
Nde I+Pst I
digest, recover
2.9 kb fragment
Ssp I (3270)
Xmn I (3105)
Ssp I(19)
Sca I (3022)
Nae I(330)
Pvu I (2876)
Pvu I (500)
Pvu II (529)
1
fi (+) origin
T7
Amp
LacZ
pHY-1
3.5Kb
Nde I (718)
EcoR I (845)
SIFN-co
T3
Pst I (1225)
ColE1 origin
Bam HI (1242)
Xba I (1433)
Pvu II (1437)
Afl III (1613)
Nde I(127)
Sac I(91)
Xba I (157)
PBAD
1 SD Sequence
EcoR V (3833)
rrnBT1T2
Cla I(921)
araC
pHY-4
4.8Kb
ScaI I(1475)
Bgl II (3208)
ColE1
Pvu II (1583)
ScaI I (2311)
Pst I (1888)
Nde I+Xba I digest
Recover 702bp
fragment
Nde I+Xba I digest
recover 4.8 kb
fragment
Sac I (91)
Nde I (127)
EcoRI (254)
Pst I(634)
BamH I(651)
PBAD
1 SD Sequence
SIFN-co
Xba I(842)
EcoRV (4518)
rrnBT1T2
araC
pHY-5
5.5Kb
Cla I(1606)
Bgl II (3893)
ColE1
Amp
ScaI I(2160)
Pvu II(2268)
ScaI I (2996)
Pst I(2573)

Figure 6-A

Circular Dichroism spectra

Tested by Analysis and Measurment Center of Sichuan University.

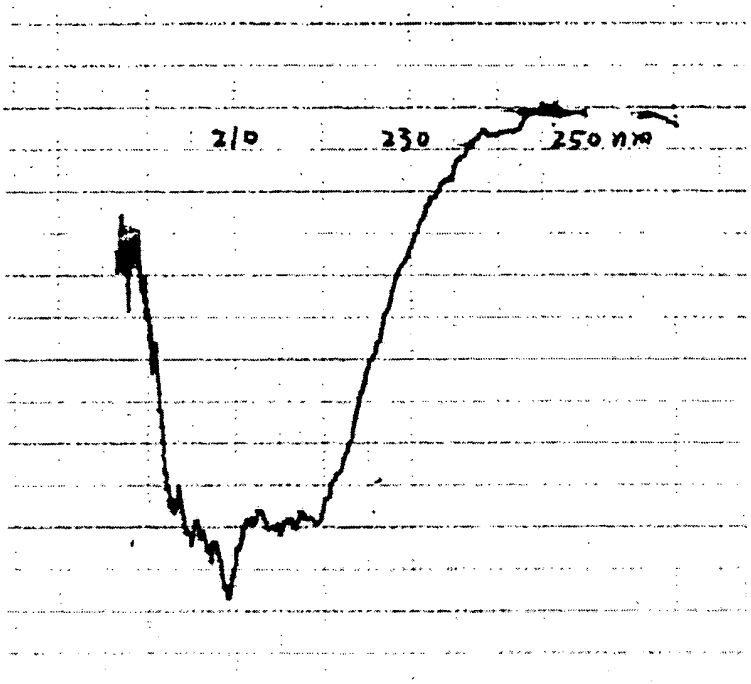

Fig 6-A Circular Dichroism spectrum of Infergen
Spectrum range: 250nm - 190nm
Sensitivity: 2 m°/cm
Light path: 0.20 cm
Equipment: Circular Dichroism J-500C
Samples :contain 30μg/ml IFN-con1, 5.9 mg/ml of NaCl and 3.8 mg/ml of Na_2PO_4, pH7.0.

Figure 6-B

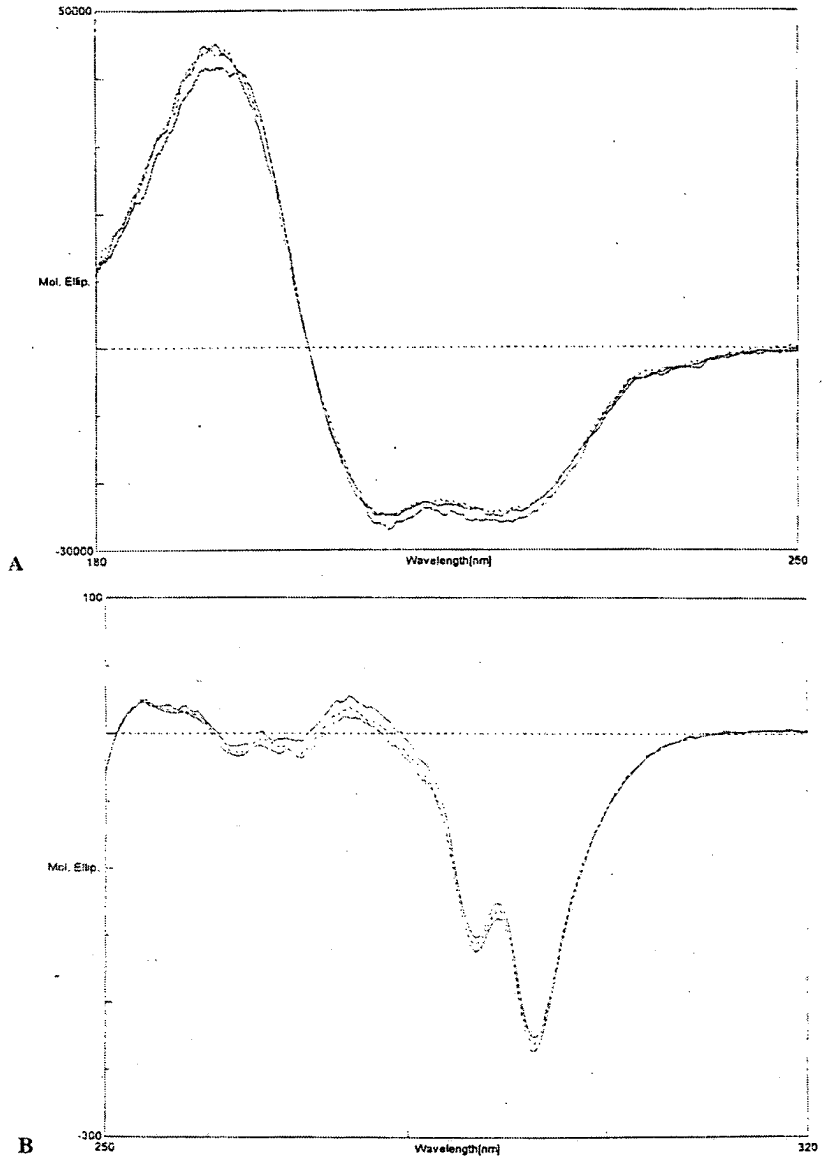

FIG. 3. Circular dichroism spectra of consensus interferon subforms. Consensus interferon was fractionated using an anion exchange column, as shown in Figure 2. Samples were dialyzed into 10 mM sodium phosphate, pH 7.4. Measurements were made on a Jasco J-170 spectopolarimeter, in a cell thermostat at 15°C. (——), acylated form; (– –), cys terminal form; (----), met terminal form. A. Far UV spectrum. B. Near UV spectrum.

Fig 6-B Circular Dichroism spectrum of Infergen From Reference[Journal of Interferon and cytokine Research. 16:489-499(1996)]

Figure 6-C

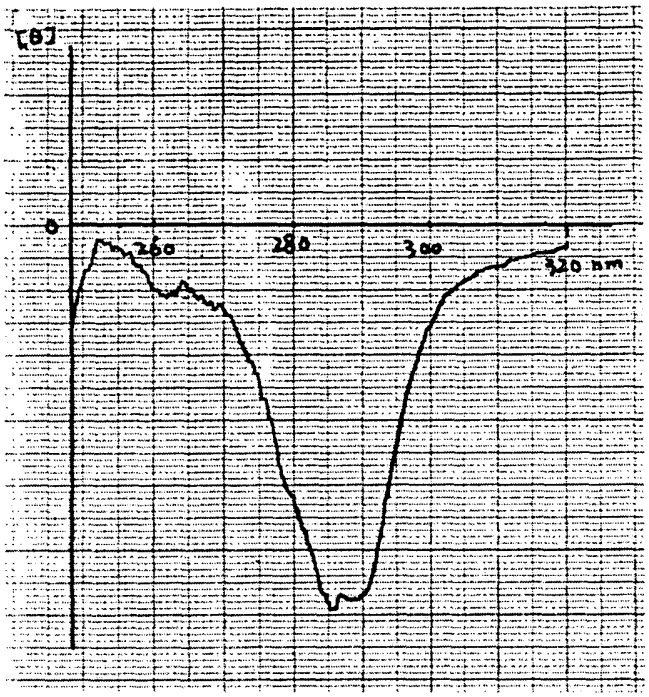

Fig 6-C Circular Dichroism spectrum of rSIFN-co

Spectrum range: 320nm-250nm

Sensitivity: 2 m° /cm

Light path: 2cm

Equipment: Circular Dichroism J-500C

Samples : contain 0.5mg/ml rSIFN-co, 5.9 mg/ml of NaCl and 3.8 mg/ml of Na_2PO_4, pH7.0.

Figure 6-D

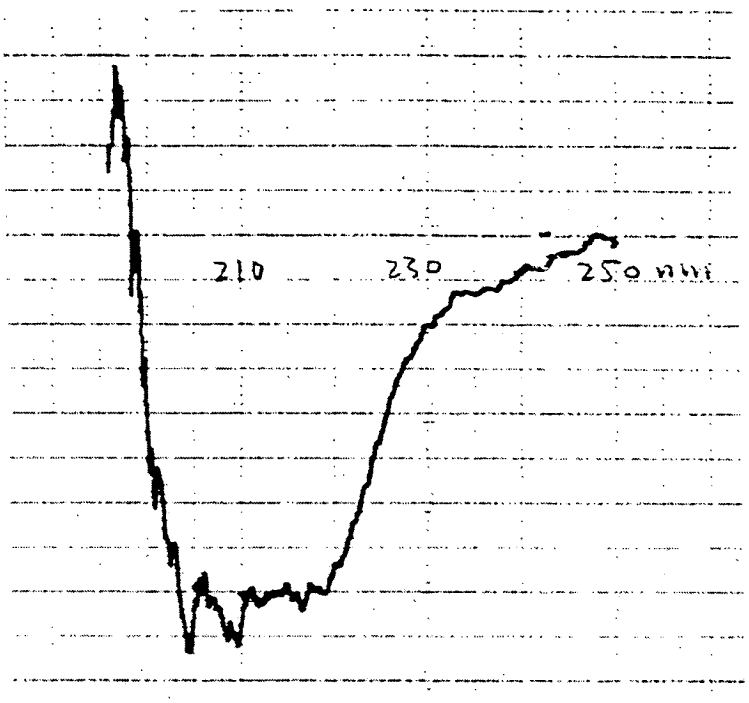

Fig 6-D Circular Dichroism spectrum of rSIFN-co

Spectrum range: 250nm – 190nm

Sensitivity: 2 m° /cm

Light path: 0.20 cm

Equipment: Circular Dichroism J-500C

Samples :contain 30μg/ml rSIFN-co, 5.9 mg/ml of NaCl and 3.8 mg/ml of Na_2PO_4, pH7.0.